



SEQUENCE LISTING

<110> E. I. du Pont de Nemours and Company
<120> Plant Glutamine Amidotransferase Homologs
<130> BB1129
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<150> 60/107,275
<151> 1998-11-05
<160> 15
<170> Microsoft Office 97
<210> 1
<211> 1956
<212> DNA
<213> Impatiens balsamia

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gaagggaaat gttcatgcag tccaatttca tcccgagaag agtggagggt tgggactttc 660
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tgaatttatg cttttaaaaa aaaaaaaaaa aaaaaa 1956

<210> 2
<211> 558

<212> PRT

<213> Impatiens balsamia

<400> 2

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Asp Tyr Gly Ala Gly Asn Val Arg Ser Val Arg Asn Ala Ile Arg Thr
35 40 45
Leu Gly Phe Asp Ile Lys Asp Val Gln Lys Pro Glu Asp Ile Leu Asn
50 55 60
Ala Lys Arg Leu Ile Phe Pro Gly Val Gly Ala Phe Ala Pro Ala Met
65 70 75 80
Asp Val Leu Ile Arg Lys Gly Leu Ala Glu Ala Leu Cys Thr Tyr Ile
85 90 95
Gln Asn Asp Arg Pro Phe Leu Gly Ile Cys Leu Gly Leu Gln Leu Leu
100 105 110
Phe Glu Ser Ser Glu Glu Asn Gly Pro Ile Gln Gly Leu Gly Leu Ile
115 120 125
Pro Gly Arg Val Gly Arg Phe Glu Ser Ser Asn Gly Leu Arg Val Pro
130 135 140
His Ile Gly Trp His Ala Leu Asp Ile Lys Glu Gly Ser Ala Ile Leu
145 150 155 160
Asp Asp Val Gly Asn Gln His Val Tyr Phe Val His Ser Tyr Arg Ala
165 170 175
Asn Ala Glu Asp Asn Lys Glu Trp Ile Ser Ser Thr Cys Ser Tyr Gly
180 185 190
Asp Asp Phe Ile Ala Ser Ile Gln Lys Gly Asn Val His Ala Val Gln
195 200 205
Phe His Pro Glu Lys Ser Gly Gly Val Gly Leu Ser Ile Leu Arg Arg
210 215 220
Phe Leu Asn Ala Asp Ser Phe Asn Asn Lys Arg Gln Lys Pro Met Asn
225 230 235 240
Gly Lys Ala Ser Lys Leu Ala Lys Arg Val Ile Ala Cys Leu Asp Val
245 250 255
Arg Ala Asn Asp Asn Gly Asp Leu Val Val Thr Lys Gly Asp Gln Tyr
260 265 270
Asp Val Arg Glu Arg Thr Glu Glu Asn Glu Val Arg Asn Leu Gly Lys
275 280 285
Pro Val Glu Leu Ala Gly Gln Tyr Tyr Leu Asp Gly Ala Asp Glu Val
290 295 300

Ser Phe Leu Asn Ile Thr Gly Phe Arg Asp Phe Pro Leu Gly Asp Leu
 305 310 315 320
 Pro Met Leu Gln Val Leu Gln Arg Ala Ser Glu Asn Val Phe Val Pro
 325 330 335
 Leu Thr Val Gly Gly Gly Ile Arg Asp Phe Thr Asp Ala Asn Gly Arg
 340 345 350
 Tyr Tyr Ser Ser Leu Glu Val Ala Ser Glu Tyr Phe Arg Ser Gly Ala
 355 360 365
 Asp Lys Val Ser Ile Gly Ser Asp Ala Val Tyr Thr Ala Glu Glu Tyr
 370 375 380
 Ile Lys Thr Gly Val Lys Thr Gly Lys Ser Ser Ile Glu Gln Ile Ser
 385 390 395 400
 Thr Val Tyr Gly Asn Gln Ala Val Val Val Ser Ile Asp Pro Arg Arg
 405 410 415
 Val Tyr Leu Arg Lys Pro Asp Glu Val Glu Phe Lys Ala Ile Lys Val
 420 425 430
 Ser His Pro Gly Pro Asn Gly Glu Glu Tyr Ala Trp Tyr Gln Cys Thr
 435 440 445
 Val Asn Gly Gly Arg Glu Gly Arg Pro Ile Gly Ala Tyr Glu Leu Ala
 450 455 460
 Lys Ala Val Glu Glu Leu Gly Ala Gly Glu Ile Leu Leu Asn Cys Ile
 465 470 475 480
 Asp Cys Asp Gly Gln Gly Lys Gly Phe Asp Ile Asp Leu Ile Lys Leu
 485 490 495
 Ile Ser Asp Ala Val Asn Ile Pro Val Ile Ala Ser Ser Gly Ala Gly
 500 505 510
 Val Ala Asp His Phe Ser Glu Val Phe Asn Glu Thr Asn Ala Ser Ala
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 Ala Leu Ala Ala Gly Ile Phe His Arg Lys Glu Val Pro Ile Lys Ala
 530 535 540
 Val Lys Glu His Leu Leu Lys Glu Gly Ile Glu Val Arg Leu
 545 550 555

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 <211> 587
 <212> DNA
 <213> Zea mays

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 ggctccttca tcgcctgctc cagcgtgcct gcgtgacata agcgtcgatt gattggcgag 180
 aaaggggacg aatgcagccg ccgttgcagg cgcagggagc aatggctaac gtcgccgcta 240
 tcctcacgtt cccctgtctc gcgggccgcc gcccggaagc gagcaaccag ccccgcggtat 300
 gcgggtccgt ctccgtctcc gtctccgtcc gtgcgtcctc cggcgcaaac acggtgactc 360
 tgctggacta cggcgcgggg aacgtacgca gcgtgcgcaa cgcaattcgc tacctcggct 420
 tcgacatccg cgacgtgcag agcccggarg acatcgtcgc cggcggaayg ggtcgtcttt 480
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<210> 4
 <211> 130
 <212> PRT
 <213> Zea mays

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 Gln Pro Arg Gly Cys Gly Ser Val Ser Val Ser Val Ser Val Arg Ala
 35 40 45

Ser Ser Gly Ala Asn Thr Val Thr Leu Leu Asp Tyr Gly Ala Gly Asn
50 55 60

Val Arg Ser Val Arg Asn Ala Ile Arg Tyr Leu Gly Phe Asp Ile Arg
65 70 75 80

Asp Val Gln Ser Pro Glu Asp Ile Val Xaa Ala Glu Xaa Val Val Phe
85 90 95

Pro Gly Val Gly Ala Phe Gly Ser Ala Met Asp Val Xaa Thr Arg Thr
100 105 110

Gly Met Xaa Asn Ala Leu Arg Glu Tyr Ile Gln Arg Glu Arg Pro Phe
115 120 125

Xaa Gly
130

<210> 5
<211> 1084
<212> DNA
<213> Zea mays

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ggtcagcttc ttgaatataa ctggtttccg tgactttcca ttgggtgatt tgccaatgct 180
agaggtagct cgttgtgcct ctgaaaagggt ttttgtgcca cttacagttg gtgggggcat 240
acgagacttc acagatgcaa atggaagata ctactcaagt ttggaggtag catcagaata 300
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aaaa 1084

<210> 6
<211> 295
<212> PRT
<213> Zea mays

<400> 6
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Ser Lys Glu Val Arg Asn Leu Gly Lys Pro Val Asp Leu Ala Ser Gln
20 25 30

Tyr Tyr Ile Asp Gly Ala Asp Glu Val Ser Phe Leu Asn Ile Thr Gly
35 40 45

Phe	Arg	Asp	Phe	Pro	Leu	Gly	Asp	Leu	Pro	Met	Leu	Glu	Val	Leu	Arg
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Cys	Ala	Ser	Glu	Lys	Val	Phe	Val	Pro	Leu	Thr	Val	Gly	Gly	Gly	Ile
65					70					75					80
Arg	Asp	Phe	Thr	Asp	Ala	Asn	Gly	Arg	Tyr	Tyr	Ser	Ser	Leu	Glu	Val
				85					90					95	
Ala	Ser	Glu	Tyr	Phe	Arg	Ser	Gly	Ala	Asp	Lys	Ile	Ser	Ile	Gly	Ser
			100					105					110		
Asp	Ala	Val	Tyr	Ala	Ala	Glu	Ala	Phe	Leu	Gln	Thr	Gly	Val	Lys	Thr
		115					120					125			
Gly	Lys	Ser	Ser	Leu	Glu	Gln	Ile	Ser	Arg	Val	Tyr	Gly	Asn	Gln	Ala
130						135					140				
Val	Val	Val	Ser	Ile	Asp	Pro	Arg	Arg	Val	Tyr	Val	Lys	Ser	Gln	Glu
145					150					155					160
Asp	Val	Pro	Phe	Lys	Thr	Val	Lys	Val	Ser	Thr	Lys	Gly	Pro	Ser	Gly
				165					170					175	
Glu	Glu	Tyr	Ala	Trp	Tyr	Gln	Cys	Thr	Val	Asn	Gly	Gly	Arg	Asp	Ser
			180					185					190		
Arg	Ala	Ile	Gly	Ala	Tyr	Glu	Leu	Ala	Lys	Ala	Val	Glu	Glu	Leu	Gly
		195					200					205			
Ala	Gly	Glu	Ile	Leu	Leu	Asn	Cys	Ile	Asp	Cys	Asp	Gly	Gln	Gly	Cys
	210					215					220				
Gly	Phe	Asp	Ile	Asp	Leu	Val	Lys	Met	Val	Ser	Asp	Ala	Val	Thr	Ile
225					230					235					240
Pro	Val	Ile	Ala	Ser	Ser	Gly	Ala	Gly	Ala	Val	Gln	His	Phe	Ser	Glu
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Ile	Phe	Glu	Lys	Thr	Asn	Ala	Ser	Ala	Ala	Leu	Ala	Ala	Gly	Ile	Phe
			260				265						270		
His	Arg	Lys	Glu	Val	Pro	Ile	Leu	Ala	Val	Lys	Glu	His	Leu	Val	Asn
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	290					295									

<210> 7
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 <212> DNA
 <213> Zea mays

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 gccagnatgt gtacttttgn tcactcctac cgcgtactgg cttcanngtg ctagtnagga 360
 aactgggggt tcctccatat ggcaactatg ggngacagct tttaatcctc catctcaa 420
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<210> 8
 <211> 86
 <212> PRT
 <213> Zea mays

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 <222> (23)

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<400> 8
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1 5 10 15
Leu Leu Phe Gly Phe Gln Xaa Gly Xaa Xaa Xaa Arg Val Ser Gly Leu
20 25 30
Gly Val Ile Ser Gly Val Xaa Arg Arg Phe Xaa Ser Ser Asn Gly Leu
35 40 45
Ile Val Pro His Val Gly Trp Asn Ala Leu Gln Xaa Thr Xaa Xaa Xaa
50 55 60
Pro Leu Leu Gln Gly Ala Asp Gly Gln Xaa Val Tyr Phe Xaa His Ser
65 70 75 80
Tyr Arg Val Leu Ala Ser
85

<210> 9
<211> 495
<212> DNA
<213> Oryza sativa

<220>
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<222> (125)

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<221> unsure
<222> (266)

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<222> (494)

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gcgngcctc tacggtcgcc gtgcgcgcgt ccggcgacgc tagcaccgtg acgctgctgg 180
actacggcgc gggcaacgtg cgcagcgtgc gcaatgccat ccgccacctc ggtttcggca 240
tcgcgcacgt gcgcagcccg gagganatcc tcgcgcgccg ccgcctcgtc ttcccggggg 300
tcggcgccctt cgggntcaag ccatggacgt cctcaacccg ctccgggatg ggcggacgcg 360
cttcncggga gtacatccgg caggggaccg ccccttcct cggnatctg gccttcgggg 420
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<210> 10
<211> 87
<212> PRT
<213> Oryza sativa

<220>
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<222> (72)

<400> 10

Met Val Ala Ala Thr Ser Ile Asn Ala Val Pro Cys Ser Ala Gly Arg
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Pro Lys Arg Arg Ser Gln Arg Arg Gly Ala Ser Thr Val Ala Val Arg
20 25 30

Ala Ser Gly Asp Ala Ser Thr Val Thr Leu Leu Asp Tyr Gly Ala Gly
35 40 45

Asn Val Arg Ser Val Arg Asn Ala Ile Arg His Leu Gly Phe Gly Ile
50 55 60

Arg Asp Val Arg Ser Pro Glu Xaa Ile Leu Ala Ala Asp Arg Leu Val
65 70 75 80

Phe Pro Gly Val Gly Ala Phe
85

<210> 11
<211> 178
<212> DNA
<213> Glycine max

<400> 11

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tcctcggggt tgacataaaa gatgtgcaaa ctccgcaaga tattctgaat gcaagtcggg 120
tagtttttcc tggtgttgga gcatttgctg ctgccatgga ggtgttaagc aaaactgg 178

<210> 12
<211> 58
<212> PRT
<213> Glycine max

<400> 12

Val Thr Leu Leu Asp Tyr Gly Ala Gly Asn Val Arg Ser Val Arg Asn
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Ala Ile Arg Phe Leu Gly Phe Asp Ile Lys Asp Val Gln Thr Pro Gln
20 25 30

Asp Ile Leu Asn Ala Ser Arg Leu Val Phe Pro Gly Val Gly Ala Phe
35 40 45

Ala Ala Ala Met Glu Val Leu Ser Lys Thr
50 55

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<212> DNA
<213> Glycine max

<220>
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<222> (276)

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aattggtgct tatgaactag caaaagcagt tgaagagctt ggtgctggtg aaatactact 180
taattgcatt gattgcgacg gtcaagggaaggaggatttgat gtagatttaa ttaagttgat 240
atcaaatgct gtaagtatcc ctgttatcgc aagtancggt gctggtgctc ctgaacactt 300
ctctgagggtg ttctataaaa caaatgcac agcagcactt gctgctggca tttttcacag 360
gaaagagggtg cctattcagt cggtaaaaga gcatttggtg aaggaaggca tagaagttcg 420
aatctgatca tatgcattta gtggtaaaat ttttgagatg cacttcataa taatcaaacc 480
ttgtacgtta tccctttttg tgtaatctaa cgaagctctc aaaatgtcaa ccttttggat 540
catgaaaaga ttttcacaac gagacctttc ctttgtaata tttttaagga aaatatattt 600
accatgtgca gcactatctc tgaacatttg ttattacaaa attatttcat gtgtcaaaaa 660
aaaaaaaaa a 671

<210> 14
<211> 141
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (92)

<400> 14
Tyr Val Lys Asp Pro Asn Asp Val Gln Leu Lys Thr Ile Arg Val Ser
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Asn Gly Gly Arg Glu Gly Arg Pro Ile Gly Ala Tyr Glu Leu Ala Lys
35 40 45
Ala Val Glu Glu Leu Gly Ala Gly Glu Ile Leu Leu Asn Cys Ile Asp
50 55 60
Cys Asp Gly Gln Gly Lys Gly Phe Asp Val Asp Leu Ile Lys Leu Ile
65 70 75 80
Ser Asn Ala Val Ser Ile Pro Val Ile Ala Ser Xaa Gly Ala Gly Ala
85 90 95
Pro Glu His Phe Ser Glu Val Phe Tyr Lys Thr Asn Ala Ser Ala Ala
100 105 110
Leu Ala Ala Gly Ile Phe His Arg Lys Glu Val Pro Ile Gln Ser Val
115 120 125
Lys Glu His Leu Leu Lys Glu Gly Ile Glu Val Arg Ile
130 135 140

<210> 15
<211> 593
<212> PRT
<213> Arabidopsis thaliana

<400> 15
Met Glu Ala Thr Ala Ala Pro Phe Ser Ser Ile Val Ser Ser Arg Gln
1 5 10 15

Asn Phe Ser Ser Ser Ser Ser Ile Arg Ala Ser Ser Pro Ala Ser Leu
 20 25 30
 Phe Leu Ser Gln Lys Ser Ile Gly Asn Val Asn Arg Lys Phe Lys Ser
 35 40 45
 Pro Arg Ser Leu Ser Val Arg Ala Ser Ser Thr Ser Asp Ser Val Val
 50 55 60
 Thr Leu Leu Asp Tyr Gly Ala Gly Asn Val Arg Ser Ile Arg Asn Ala
 65 70 75 80
 Leu Arg His Leu Gly Phe Ser Ile Lys Asp Val Gln Thr Pro Gly Asp
 85 90 95
 Ile Leu Asn Ala Asp Arg Leu Ile Phe Pro Gly Val Gly Pro Phe Ala
 100 105 110
 Pro Ala Met Asp Val Leu Asn Arg Thr Gly Met Ala Glu Ala Leu Cys
 115 120 125
 Lys Tyr Ile Glu Asn Asp Arg Pro Phe Leu Gly Ile Cys Leu Gly Leu
 130 135 140
 Gln Leu Leu Phe Asp Ser Ser Glu Gln Asn Gly Pro Val Lys Gly Leu
 145 150 155 160
 Gly Val Ile Pro Gly Ile Val Gly Arg Phe Asp Ala Ser Ala Gly Ile
 165 170 175
 Arg Val Pro His Ile Gly Trp Asn Ala Leu Gln Val Gly Lys Asp Ser
 180 185 190
 Glu Ile Leu Asp Asp Val Gly Asn Arg His Val Tyr Phe Val His Ser
 195 200 205
 Tyr Arg Ala Ile Pro Ser Asp Glu Asn Lys Asp Trp Ile Ser Ser Thr
 210 215 220
 Cys Asn Tyr Gly Glu Ser Phe Ile Ser Ser Ile Arg Arg Gly Asn Val
 225 230 235 240
 His Ala Val Gln Phe His Pro Glu Lys Ser Gly Glu Val Gly Leu Ser
 245 250 255
 Val Leu Arg Arg Phe Leu His Pro Lys Leu Pro Ala Thr Gln Lys Pro
 260 265 270
 Met Glu Gly Lys Ala Ser Lys Leu Ala Lys Arg Val Ile Ala Cys Leu
 275 280 285
 Asp Val Arg Thr Asn Asp Lys Gly Asp Leu Val Val Thr Lys Gly Asp
 290 295 300
 Gln Tyr Asp Val Arg Glu Gln Ser Asn Glu Asn Glu Val Arg Asn Leu
 305 310 315 320
 Gly Lys Pro Val Asp Leu Ala Gly Gln Tyr Tyr Lys Asp Gly Ala Asp
 325 330 335

Glu Ile Ser Phe Leu Asn Ile Thr Gly Phe Arg Asp Phe Pro Leu Gly
 340 345 350
 Asp Leu Pro Met Ile Gln Val Leu Arg Gln Thr Ser Lys Asn Val Phe
 355 360 365
 Val Pro Leu Thr Val Gly Gly Gly Ile Arg Asp Phe Thr Asp Ala Ser
 370 375 380
 Gly Arg Tyr Tyr Ser Ser Leu Glu Val Ala Ala Glu Tyr Phe Arg Ser
 385 390 395 400
 Gly Ala Asp Lys Met Ser Ile Gly Ser Asp Ala Val Phe Ala Ala Glu
 405 410 415
 Glu Phe Ile Lys Ser Gly Val Lys Thr Gly Lys Ser Ser Leu Glu Gln
 420 425 430
 Ile Ser Arg Val Tyr Gly Asn Gln Ala Val Val Val Ser Ile Asp Pro
 435 440 445
 Arg Arg Val Tyr Val Asn His Pro Asp Asp Val Pro Tyr Lys Val Ile
 450 455 460
 Arg Val Thr Asn Pro Gly Pro Asn Gly Glu Glu Tyr Ala Trp Tyr Gln
 465 470 475 480
 Cys Thr Val Ser Gly Gly Gln Glu Gly Arg Pro Ile Gly Ala Phe Glu
 485 490 495
 Leu Ala Lys Ala Val Glu Glu Leu Gly Ala Gly Glu Ile Leu Leu Asn
 500 505 510
 Cys Ile Asn Cys Asp Gly Gln Gly Lys Gly Phe Asp Ile Asp Leu Val
 515 520 525
 Lys Leu Ile Ser Asp Ser Val Gly Ile Pro Val Ile Ala Ser Ser Gly
 530 535 540
 Ala Gly Thr Pro Asp His Phe Ser Glu Val Phe Glu Glu Asp Lys Arg
 545 550 555 560
 Ile Cys Arg Ala Cys Cys Arg His Phe Pro Pro Glu Arg Gly Tyr Gln
 565 570 575
 Ser Gln Ser Val Lys Glu His Leu Gln Glu Glu Arg Ile Glu Val Arg
 580 585 590
 Ile